



Does Not Comply
Corrected Diskette Needed

OIPPE

RAW SEQUENCE LISTING

DATE: 02/13/2003

PATENT APPLICATION: US/09/940,316B

TIME: 13:57:40

Input Set : D:\30062-20026.txt

Output Set: N:\CRF4\02132003\I940316B.raw

3 <110> APPLICANT: KOSAN BIOSCIENCES, Inc.
 4 REEVES, CHRISTOPHER
 5 CHU, DANIEL
 6 KHOSLA, CHAITAN
 7 SANTI, DANIEL
 8 WU, KAI
 10 <120> TITLE OF INVENTION: POLYKETIDES ENCODING THE fkbA GENE OF THE FK-520 POLYKETIDE SYNTHASE
 11 GENE CLUSTER
 13 <130> FILE REFERENCE: 30062-20026.11
 15 <140> CURRENT APPLICATION NUMBER: 09/940,316B
C--> 16 <141> CURRENT FILING DATE: 2003-02-05
 18 <150> PRIOR APPLICATION NUMBER: 09/410,551
 19 <151> PRIOR FILING DATE: 1999-10-01
 21 <150> PRIOR APPLICATION NUMBER: US 60/139,650
 22 <151> PRIOR FILING DATE: 1999-06-17
 24 <150> PRIOR APPLICATION NUMBER: US 60/123,810
 25 <151> PRIOR FILING DATE: 1999-03-11
 27 <150> PRIOR APPLICATION NUMBER: US 60/102,748
 28 <151> PRIOR FILING DATE: 1998-10-02
 30 <160> NUMBER OF SEQ ID NOS: 72
 32 <170> SOFTWARE: FastSEQ for Windows Version 4.0

ERRORED SEQUENCES

4615 <210> SEQ ID NO: 21
 4616 <211> LENGTH: 1482
 4617 <212> TYPE: PRT
 4618 <213> ORGANISM: Artificial Sequence
 4620 <220> FEATURE:
 4621 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic PKS
 4622 synthase fragment
 4624 <400> SEQUENCE: 21
 4625 Gln Leu Ala Glu Ala Leu Leu Thr Leu Val Arg Glu Ser Thr Ala Ala
 4626 1 5 10 15
 4628 Val Leu Gly His Val Gly Gly Glu Asp Ile Pro Ala Thr Ala Ala Phe
 4629 20 25 30
 4631 Lys Asp Leu Gly Ile Asp Ser Leu Thr Ala Val Gln Leu Arg Asn Ala
 4632 35 40 45
 4634 Leu Thr Glu Ala Thr Gly Val Arg Leu Asn Ala Thr Ala Val Phe Asp
 4635 50 55 60
 4637 Phe Pro Thr Pro His Val Leu Ala Gly Lys Leu Gly Asp Glu Leu Thr
 4638 65 70 75 80

*Misalignment of amino
 numbers throughout. Only
 errored portion of a sequence
 shown.*

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```

4787 Ala Leu Ala His Leu Tyr Val Asn Gly Val Thr Val Asp Trp Pro Ala
4788 865 870 875 880
4790 Leu Leu Gly Asp Ala Pro Ala Thr Arg Val Leu Asp Leu Pro Thr Tyr
4791 885 890 895
4793 Ala Phe Gln His Gln Arg Tyr Trp Leu Glu Ser Ala Arg Pro Ala Ala
4794 900 905 910
4796 Ser Asp Ala Gly His Pro Val Leu Gly Ser Gly Ile Ala Leu Ala Gly
4797 915 920 925
4799 Ser Pro Gly Arg Val Phe Thr Gly Ser Val Pro Thr Gly Ala Asp Arg
4800 930 935 940
4802 Ala Val Phe Val Ala Glu Leu Ala Leu Ala Ala Asp Ala Val Asp
4803 945 950 955 960
4805 Cys Ala Thr Val Glu Arg Leu Asp Ile Ala Ser Val Pro Gly Arg Pro
4806 965 970 975
4808 Gly His Gly Arg Thr Thr Val Gln Thr Trp Val Asp Glu Pro Ala Asp
4809 980 985 990
4811 Asp Gly Arg Arg Arg Phe Thr Val His Thr Arg Thr Gly Asp Ala Pro
4812 995 1000 1005
4814 Trp Thr Leu His Ala Glu Gly Val Leu Arg Pro His Gly Thr Ala Leu
4815 1010 1015 1020
4817 Pro Asp Ala Ala Asp Ala Glu Trp Pro Pro Pro Gly Ala Val Pro Ala
4818 1025 1030 1035 1040
4820 Asp Gly Leu Pro Gly Val Trp Arg Arg Gly Asp Gln Val Phe Ala Glu
4821 1045 1050 1055
4823 Ala Glu Val Asp Gly Pro Asp Gly Phe Val Val His Pro Asp Leu Leu
4824 1060 1065 1070
4826 Asp Ala Val Phe Ser Ala Val Gly Asp Gly Ser Arg Gln Pro Ala Gly
4827 1075 1080 1085
4829 Trp Arg Asp Leu Thr Val His Ala Ser Asp Ala Thr Val Leu Arg Ala
4830 1090 1095 1100
4832 Cys Leu Thr Arg Arg Thr Asp Gly Ala Met Gly Phe Ala Ala Phe Asp
4833 1105 1110 1115 1120
4835 Gly Ala Gly Leu Pro Val Leu Thr Ala Glu Ala Val Thr Leu Arg Glu
4836 1125 1130 1135
4838 Val Ala Ser Pro Ser Gly Ser Glu Glu Ser Asp Gly Leu His Arg Leu
E--> 4839 1140 1145 1150
4841 Glu Trp Leu Ala Val Ala Glu Ala Val Tyr Asp Gly Asp Leu Pro Glu
E--> 4842 1155 1160 1165
4844 Gly His Val Leu Ile Thr Ala Ala His Pro Asp Asp Pro Glu Asp Ile
E--> 4845 1170 1175 1180
4847 Pro Thr Arg Ala His Thr Arg Ala Thr Arg Val Leu Thr Ala Leu Gln
E--> 4848 1185 1190 1195 1200
4850 His His Leu Thr Thr Thr Asp His Thr Leu Ile Val His Thr Thr Thr
E--> 4851 1205 1210 1215
4853 Asp Pro Ala Gly Ala Thr Val Thr Gly Leu Thr Arg Thr Ala Gln Asn
4854 1220 1225 1230
4856 Glu His Pro His Arg Ile Arg Leu Ile Glu Thr Asp His Pro His Thr
4857 1235 1240 1245
4859 Pro Leu Pro Leu Ala Gln Leu Ala Thr Leu Asp His Pro His Leu Arg

```

Move to the left so that the
last digit does not fall below
the first letter of the next
amino.

- same

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Input Set : D:\30062-20026.txt

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```

4860      1250      1255      1260
4862 Leu Thr His His Thr Leu His His Pro His Leu Thr Pro Leu His Thr
4863 1265      1270      1275      1280
4865 Thr Thr Pro Pro Thr Thr Thr Pro Leu Asn Pro Glu His Ala Ile Ile
4866      1285      1290      1295
4868 Ile Thr Gly Gly Ser Gly Thr Leu Ala Gly Ile Leu Ala Arg His Leu
4869      1300      1305      1310
4871 Asn His Pro His Thr Tyr Leu Leu Ser Arg Thr Pro Pro Pro Asp Ala
4872      1315      1320      1325
4874 Thr Pro Gly Thr His Leu Pro Cys Asp Val Gly Asp Pro His Gln Leu
4875      1330      1335      1340
4877 Ala Thr Thr Leu Thr His Ile Pro Gln Pro Leu Thr Ala Ile Phe His
4878 1345      1350      1355      1360
4880 Thr Ala Ala Thr Leu Asp Asp Gly Ile Leu His Ala Leu Thr Pro Asp
4881      1365      1370      1375
4883 Arg Leu Thr Thr Val Leu His Pro Lys Ala Asn Ala Ala Trp His Leu
4884      1380      1385      1390
4886 His His Leu Thr Gln Asn Gln Pro Leu Thr His Phe Val Leu Tyr Ser
4887      1395      1400      1405
4889 Ser Ala Ala Ala Val Leu Gly Ser Pro Gly Gln Gly Asn Tyr Ala Ala
4890      1410      1415      1420
4892 Ala Asn Ala Phe Leu Asp Ala Leu Ala Thr His Arg His Thr Leu Gly
4893 1425      1430      1435      1440
4895 Gln Pro Ala Thr Ser Ile Ala Trp Gly Met Trp His Thr Thr Ser Thr
4896      1445      1450      1455
4898 Leu Thr Gly Gln Leu Asp Asp Ala Asp Arg Asp Arg Ile Arg Arg Gly
4899      1460      1465      1470
4901 Gly Phe Leu Pro Ile Thr Asp Asp Glu Gly
4902      1475      1480
6722 <210> SEQ ID NO: 27
6723 <211> LENGTH: 1557
6724 <212> TYPE: PRT
6725 <213> ORGANISM: Artificial Sequence
6727 <220> FEATURE:
6728 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic PKS
6729      synthase fragment
6731 <400> SEQUENCE: 27
6732 Met Arg Leu Tyr Glu Ala Ala Arg Arg Thr Gly Ser Pro Val Val Val
6733 1      5      10      15
6735 Ala Ala Ala Leu Asp Asp Ala Pro Asp Val Pro Leu Leu Arg Gly Leu
6736      20      25      30
6738 Arg Arg Thr Thr Val Arg Arg Ala Ala Val Arg Glu Arg Ser Leu Ala
6739      35      40      45
6741 Asp Arg Ser Pro Cys Cys Pro Thr Thr Ser Ala Pro Thr Pro Pro Ser
6742      50      55      60
6744 Arg Ser Ser Trp Asn Ser Thr Ala Thr Val Leu Gly His Leu Gly Ala
6745 65      70      75      80
6747 Glu Asp Ile Pro Ala Thr Thr Thr Phe Lys Glu Leu Gly Ile Asp Ser
6748      85      90      95

```

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```

6970 1265          1270          1275          1280
6972 Val His Thr Thr Thr Asp Pro Pro Gly Ala Ala Val Thr Gly Leu Thr
6973          1285          1290          1295
6975 Arg Thr Ala Gln Asn Glu His Pro Gly Arg Ile His Leu Ile Glu Thr
6976          1300          1305          1310
6978 His His Pro His Thr Pro Leu Pro Leu Thr Gln Leu Thr Thr Leu His
6979          1315          1320          1325
6981 Gln Pro His Leu Arg Leu Thr Asn Asn Thr Leu His Thr Pro His Leu
6982          1330          1335          1340
6984 Thr Pro Ile Thr Thr His His Asn Thr Thr Thr Thr Thr Pro Asn Thr
6985 1345          1350          1355          1360
6987 Pro Pro Leu Asn Pro Asn His Ala Ile Leu Ile Thr Gly Gly Ser Gly
6988          1365          1370          1375
6990 Thr Leu Ala Gly Ile Leu Ala Arg His Leu Asn His Pro His Thr Tyr
6991          1380          1385          1390
6993 Leu Leu Ser Arg Thr Pro Pro Pro Pro Thr Thr Pro Gly Thr His Ile
6994          1395          1400          1405
6996 Pro Cys Asp Leu Thr Asp Pro Thr Gln Ile Thr Gln Ala Leu Thr His
6997          1410          1415          1420
6999 Ile Pro Gln Pro Leu Thr Gly Ile Phe His Thr Ala Ala Thr Leu Asp
E--> 7000 1425 1430 1435 1440 - same
7002 Asp Ala Thr Leu Thr Asn Leu Thr Pro Gln His Leu Thr Thr Thr Leu
7003          1445          1450          1455
7005 Gln Pro Lys Ala Asp Ala Ala Trp His Leu His His His Thr Gln Asn
7006          1460          1465          1470
7008 Gln Pro Leu Thr His Phe Val Leu Tyr Ser Ser Ala Ala Ala Thr Leu
7009          1475          1480          1485
7011 Gly Ser Pro Gly Gln Ala Asn Tyr Ala Ala Ala Asn Ala Phe Leu Asp
7012          1490          1495          1500
7014 Ala Leu Ala Thr His Arg His Thr Gln Gly Gln Pro Ala Thr Thr Ile
7015 1505          1510          1515          1520
7017 Ala Trp Gly Met Trp His Thr Thr Thr Thr Leu Thr Ser Gln Leu Thr
7018          1525          1530          1535
7020 Asp Ser Asp Arg Asp Arg Ile Arg Arg Gly Gly Phe Leu Pro Ile Ser
7021          1540          1545          1550
7023 Asp Asp Glu Gly Met
7024          1555
8164 <210> SEQ ID NO: 31
8165 <211> LENGTH: 1578
8166 <212> TYPE: PRT
8167 <213> ORGANISM: Artificial Sequence
8169 <220> FEATURE:
8170 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic PKS
8171      synthase fragment
8173 <400> SEQUENCE: 31
8174 Met Arg Leu Tyr Glu Ala Ala Arg Arg Thr Gly Ser Pro Val Val Val
8175 1          5          10          15
8177 Ala Ala Ala Leu Asp Asp Ala Pro Asp Val Pro Leu Leu Arg Gly Leu
8178          20          25          30

```

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```

8400          1205          1210          1215
8402 Gly Glu Val Ala Ser Ala Gly Gly Ser Asp Glu Ser Asp Gly Leu Leu
8403          1220          1225          1230
8405 Arg Leu Glu Trp Leu Pro Val Ala Glu Ala His Tyr Asp Gly Ala Asp
8406          1235          1240          1245
8408 Glu Leu Pro Glu Gly Tyr Thr Leu Ile Thr Ala Thr His Pro Asp Asp
8409          1250          1255          1260
8411 Pro Asp Asp Pro Thr Asn Pro His Asn Thr Pro Thr Arg Thr His Thr
8412 1265          1270          1275          1280
8414 Gln Thr Thr Arg Val Leu Thr Ala Leu Gln His His Leu Ile Thr Thr
8415          1285          1290          1295
8417 Asn His Thr Leu Ile Val His Thr Thr Thr Asp Pro Pro Gly Ala Ala
8418          1300          1305          1310
8420 Val Thr Gly Leu Thr Arg Thr Ala Gln Asn Glu His Pro Gly Arg Ile
8421          1315          1320          1325
8423 His Leu Ile Glu Thr His His Pro His Thr Pro Leu Pro Leu Thr Gln
8424          1330          1335          1340
8426 Leu Thr Thr Leu His Gln Pro His Leu Arg Leu Thr Asn Asn Thr Leu
8427 1345          1350          1355          1360
8429 His Thr Pro His Leu Thr Pro Ile Thr Thr His His Asn Thr Thr Thr
8430          1365          1370          1375
8432 Thr Thr Pro Asn Thr Pro Pro Leu Asn Pro Asn His Ala Ile Leu Ile
8433          1380          1385          1390
8435 Thr Gly Gly Ser Gly Thr Leu Ala Gly Ile Leu Ala Arg His Leu Asn
8436          1395          1400          1405
8438 His Pro His Thr Tyr Leu Leu Ser Arg Thr Pro Pro Pro Pro Thr Thr
8439          1410          1415          1420
8441 Pro Gly Thr His Ile Pro Cys Asp Leu Thr Asp Pro Thr Gln Ile Thr
8442 1425          1430          1435          1440
8444 Gln Ala Leu Thr His Ile Pro Gln Pro Leu Thr Gly Ile Phe His Thr
8445          1445          1450          1455
8447 Ala Ala Thr Leu Asp Asp Ala Thr Leu Thr Asn Leu Thr Pro Gln His
8448          1460          1465          1470
8450 Leu Thr Thr Thr Leu Gln Pro Lys Ala Asp Ala Ala Trp His Leu His
8451          1475          1480          1485
8453 His His Thr Gln Asn Gln Pro Leu Thr His Phe Val Leu Tyr Ser Ser
8454          1490          1495          1500
8456 Ala Ala Ala Thr Leu Gly Ser Pro Gly Gln Ala Asn Tyr Ala Ala Ala
8457 1505          1510          1515          1520
8459 Asn Ala Phe Leu Asp Ala Leu Ala Thr His Arg His Thr Gln Gly Gln
8460          1525          1530          1535
8462 Pro Ala Thr Thr Ile Ala Trp Gly Met Trp His Thr Thr Thr Thr Leu
E--> 8463 1540 ←1545 ←1550 - some error
8465 Thr Ser Gln Leu Thr Asp Ser Asp Arg Asp Arg Ile Arg Arg Gly Gly
8466          1555          1560          1565
8468 Phe Leu Pro Ile Ser Asp Asp Glu Gly Met
8469          1570          1575
8891 <210> SEQ ID NO: 33
8892 <211> LENGTH: 1605

```

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Output Set: N:\CRF4\02132003\I940316B.raw

```

8893 <212> TYPE: PRT
8894 <213> ORGANISM: Artificial Sequence
8896 <220> FEATURE:
8897 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic PKS
8898     synthase fragment
8900 <400> SEQUENCE: 33
8901 Met Arg Leu Tyr Glu Ala Ala Arg Arg Thr Gly Ser Pro Val Val Val
8902   1           5           10           15
8904 Ala Ala Ala Leu Asp Asp Ala Pro Asp Val Pro Leu Leu Arg Gly Leu
8905           20           25           30
8907 Arg Arg Thr Thr Val Arg Arg Ala Ala Val Arg Glu Arg Ser Leu Ala
8908           35           40           45
8910 Asp Arg Ser Pro Cys Cys Pro Thr Thr Ser Ala Pro Thr Pro Pro Ser
8911           50           55           60
8913 Arg Ser Ser Trp Asn Ser Thr Ala Thr Val Leu Gly His Leu Gly Ala
8914   65           70           75           80
8916 Glu Asp Ile Pro Ala Thr Thr Thr Phe Lys Glu Leu Gly Ile Asp Ser
8917           85           90           95
8919 Leu Thr Ala Val Gln Leu Arg Asn Ala Leu Thr Thr Ala Thr Gly Val
8920           100          105          110
8922 Arg Leu Asn Ala Thr Ala Val Phe Asp Phe Pro Thr Pro Arg Ala Leu
8923           115          120          125
8925 Ala Ala Arg Leu Gly Asp Glu Leu Ala Gly Thr Arg Ala Pro Val Ala
8926           130          135          140
8928 Ala Arg Thr Ala Ala Thr Ala Ala Ala His Asp Glu Pro Leu Ala Ile
8929  145          150          155          160
8931 Val Gly Met Ala Cys Arg Leu Pro Gly Gly Val Ala Ser Pro Gln Glu
8932           165          170          175
8934 Leu Trp Arg Leu Val Ala Ser Gly Thr Asp Ala Ile Thr Glu Phe Pro
8935           180          185          190
8937 Ala Asp Arg Gly Trp Asp Val Asp Ala Leu Tyr Asp Pro Asp Pro Asp
8938           195          200          205
8940 Ala Ile Gly Lys Thr Phe Val Arg His Gly Gly Phe Leu Asp Gly Ala
8941           210          215          220
8943 Thr Gly Phe Asp Ala Ala Phe Phe Gly Ile Ser Pro Arg Glu Ala Leu
8944  225          230          235          240
8946 Ala Met Asp Pro Gln Gln Arg Val Leu Leu Glu Thr Ser Trp Glu Ala
8947           245          250          255
8949 Phe Glu Ser Ala Gly Ile Thr Pro Asp Ala Ala Arg Gly Ser Asp Thr
8950           260          265          270
8952 Gly Val Phe Ile Gly Ala Phe Ser Tyr Gly Tyr Gly Thr Gly Ala Asp
8953           275          280          285
8955 Thr Asn Gly Phe Gly Ala Thr Gly Ser Gln Thr Ser Val Leu Ser Gly
8956           290          295          300
8958 Arg Leu Ser Tyr Phe Tyr Gly Leu Glu Gly Pro Ser Val Thr Val Asp
8959  305          310          315          320
8961 Thr Ala Cys Ser Ser Ser Leu Val Ala Leu His Gln Ala Gly Gln Ser
8962           325          330          335
8964 Leu Arg Ser Gly Glu Cys Ser Leu Ala Leu Val Gly Gly Val Thr Val

```

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Input Set : D:\30062-20026.txt

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9186 Gln Pro Leu Thr His Phe Val Leu Tyr Ser Ser Ala Ala Ala Thr Leu
 9187 1525 1530 1535
 9189 Gly Ser Pro Gly Gln Ala Asn Tyr Ala Ala Ala Asn Ala Phe Leu Asp
 9190 1540 1545 1550
 9192 Ala Leu Ala Thr His Arg His Thr Gln Gly Gln Pro Ala Thr Thr Ile
 E--> 9193 ←1555 ←1560 ←1565
 9195 Ala Trp Gly Met Trp His Thr Thr Thr Thr Leu Thr Ser Gln Leu Thr
 E--> 9196 1570 1575 1580
 9198 Asp Ser Asp Arg Asp Arg Ile Arg Arg Gly Gly Phe Leu Pro Ile Ser
 E--> 9199 1585 1590 1595 1600
 9201 Asp Asp Glu Gly Met
 E--> 9202 1605
 9979 <210> SEQ ID NO: 72
 9980 <211> LENGTH: 6396
 9981 <212> TYPE: PRT
 9982 <213> ORGANISM: Streptomyces hygroscopicus
 9984 <400> SEQUENCE: 72
 9985 Met Pro Glu Gln Asp Lys Thr Val Glu Tyr Leu Arg Trp Ala Thr Ala
 9986 1 5 10 15
 9987 Glu Leu Gln Lys Thr Arg Ala Glu Leu Ala Ala His Ser Glu Pro Leu
 9988 20 25 30
 9989 Ala Ile Val Gly Met Ala Cys Arg Leu Pro Gly Gly Val Ala Ser Pro
 9990 35 40 45
 9991 Glu Asp Leu Trp Gln Leu Leu Glu Ser Gly Gly Asp Gly Ile Thr Ala
 9992 50 55 60
 9993 Phe Pro Thr Asp Arg Gly Trp Glu Thr Thr Ala Asp Gly Arg Gly Gly
 9994 65 70 75 80
 9995 Phe Leu Thr Gly Ala Ala Gly Phe Asp Ala Ala Phe Phe Gly Ile Ser
 9996 85 90 95
 9997 Pro Arg Glu Ala Leu Ala Met Asp Pro Gln Gln Arg Leu Ala Leu Glu
 9998 100 105 110
 9999 Thr Ser Trp Glu Ala Phe Glu His Ala Gly Ile Asp Pro Gln Thr Leu
 10000 115 120 125
 10001 Arg Gly Ser Asp Thr Gly Val Phe Leu Gly Ala Phe Phe Gln Gly Tyr
 10002 130 135 140
 10003 Gly Ile Gly Ala Asp Phe Asp Gly Tyr Gly Thr Thr Ser Ile His Thr
 10004 145 150 155 160
 10005 Ser Val Leu Ser Gly Arg Leu Ala Tyr Phe Tyr Gly Leu Glu Gly Pro
 10006 165 170 175
 10007 Ala Val Thr Val Asp Thr Ala Cys Ser Ser Ser Leu Val Ala Leu His
 10008 180 185 190
 10009 Gln Ala Gly Gln Ser Leu Arg Ser Gly Glu Cys Ser Leu Ala Leu Val
 10010 195 200 205
 10011 Gly Gly Val Thr Val Met Ala Ser Pro Ala Gly Phe Ala Asp Phe Ser
 10012 210 215 220
 10013 Glu Gln Gly Gly Leu Ala Pro Asp Ala Arg Cys Lys Ala Phe Ala Glu
 10014 225 230 235 240
 10015 Ala Ala Asp Gly Thr Gly Phe Ala Glu Gly Ser Gly Val Leu Ile Val
 10016 245 250 255

amino numbers
 misaligned
 — some

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TIME: 13:57:41

Input Set : D:\30062-20026.txt

Output Set: N:\CRF4\02132003\I940316B.raw

```

10213 Leu Gly His Val Gly Gly Glu Asp Ile Pro Ala Thr Ala Ala Phe Lys
10214 1825 1830 1835 1840
10215 Asp Leu Gly Ile Asp Ser Leu Thr Ala Val Gln Leu Arg Asn Ala Leu
10216 1845 1850 1855
10217 Thr Glu Ala Thr Gly Val Arg Leu Asn Ala Thr Ala Val Phe Asp Phe
10218 1860 1865 1870
10219 Pro Thr Pro His Val Leu Ala Gly Lys Leu Gly Asp Glu Leu Thr Gly
10220 1875 1880 1885
10221 Thr Arg Ala Pro Val Val Pro Arg Thr Ala Ala Thr Ala Gly Ala His
10222 1890 1895 1900
10223 Asp Glu Pro Leu Ala Ile Val Gly Met Ala Cys Arg Leu Pro Gly Gly
10224 1905 1910 1915 1920
10225 Val Ala Ser Pro Glu Glu Leu Trp His Leu Val Ala Ser Gly Thr Asp
10226 1925 1930 1935
10227 Ala Ile Thr Glu Phe Pro Thr Asp Arg Gly Trp Asp Val Asp Ala Ile
10228 1940 1945 1950
10229 Tyr Asp Pro Asp Pro Asp Ala Ile Gly Lys Thr Phe Val Arg His Gly
10230 1955 1960 1965
10231 Gly Phe Leu Thr Gly Ala Thr Gly Phe Asp Ala Ala Phe Phe Gly Ile
10232 1970 1975 1980
10233 Ser Pro Arg Glu Ala Leu Ala Met Asp Pro Gln Gln Arg Val Leu Leu
10234 1985 1990 1995 2000
10235 Glu Thr Ser Trp Glu Ala Phe Glu Ser Ala Gly Ile Thr Pro Asp Ser
10236 2005 2010 2015
10237 Thr Arg Gly Ser Asp Thr Gly Val Phe Val Gly Ala Phe Ser Tyr Gly
10238 2020 2025 2030
10239 Tyr Gly Thr Gly Ala Asp Thr Asp Gly Phe Gly Ala Thr Gly Ser Gln
10240 2035 2040 2045
10241 Thr Ser Val Leu Ser Gly Arg Leu Ser Tyr Phe Tyr Gly Leu Glu Gly
10242 2050 2055 2060
10243 Pro Ala Val Thr Val Asp Thr Ala Cys Ser Ser Ser Leu Val Ala Leu
E--> 10244 2065 2070 2075 2080 add
10245 His Gln Ala Gly Gln Ser Leu Arg Ser Gly Glu Cys Ser Leu Ala Leu
10246 2085 2090 2095
10247 Val Gly Gly Val Thr Val Met Ala Ser Pro Gly Gly Phe Val Glu Phe
10248 2100 2105 2110
10249 Ser Arg Gln Arg Gly Leu Ala Pro Asp Gly Arg Ala Lys Ala Phe Gly
10250 2115 2120 2125
10251 Ala Gly Ala Asp Gly Thr Ser Phe Ala Glu Gly Ala Gly Val Leu Ile
10252 2130 2135 2140
10253 Val Glu Arg Leu Ser Asp Ala Glu Arg Asn Gly His Thr Val Leu Ala
10254 2145 2150 2155 2160
10255 Val Val Arg Gly Ser Ala Val Asn Gln Asp Gly Ala Ser Asn Gly Leu
10256 2165 2170 2175
10257 Ser Ala Pro Asn Gly Pro Ser Gln Glu Arg Val Ile Arg Gln Ala Leu
10258 2180 2185 2190
10259 Ala Asn Ala Gly Leu Thr Pro Ala Asp Val Asp Ala Val Glu Ala His
10260 2195 2200 2205
10261 Gly Thr Gly Thr Arg Leu Gly Asp Pro Ile Glu Ala Gln Ala Val Leu

```


VERIFICATION SUMMARY

DATE: 02/13/2003

PATENT APPLICATION: US/09/940,316B

TIME: 13:57:42

Input Set : D:\30062-20026.txt

Output Set: N:\CRF4\02132003\I940316B.raw

L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:2519 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:4839 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:21
M:332 Repeated in SeqNo=21
L:7000 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:27
L:7351 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:28
L:8463 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:31
L:9193 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:33
M:332 Repeated in SeqNo=33
L:10244 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:72